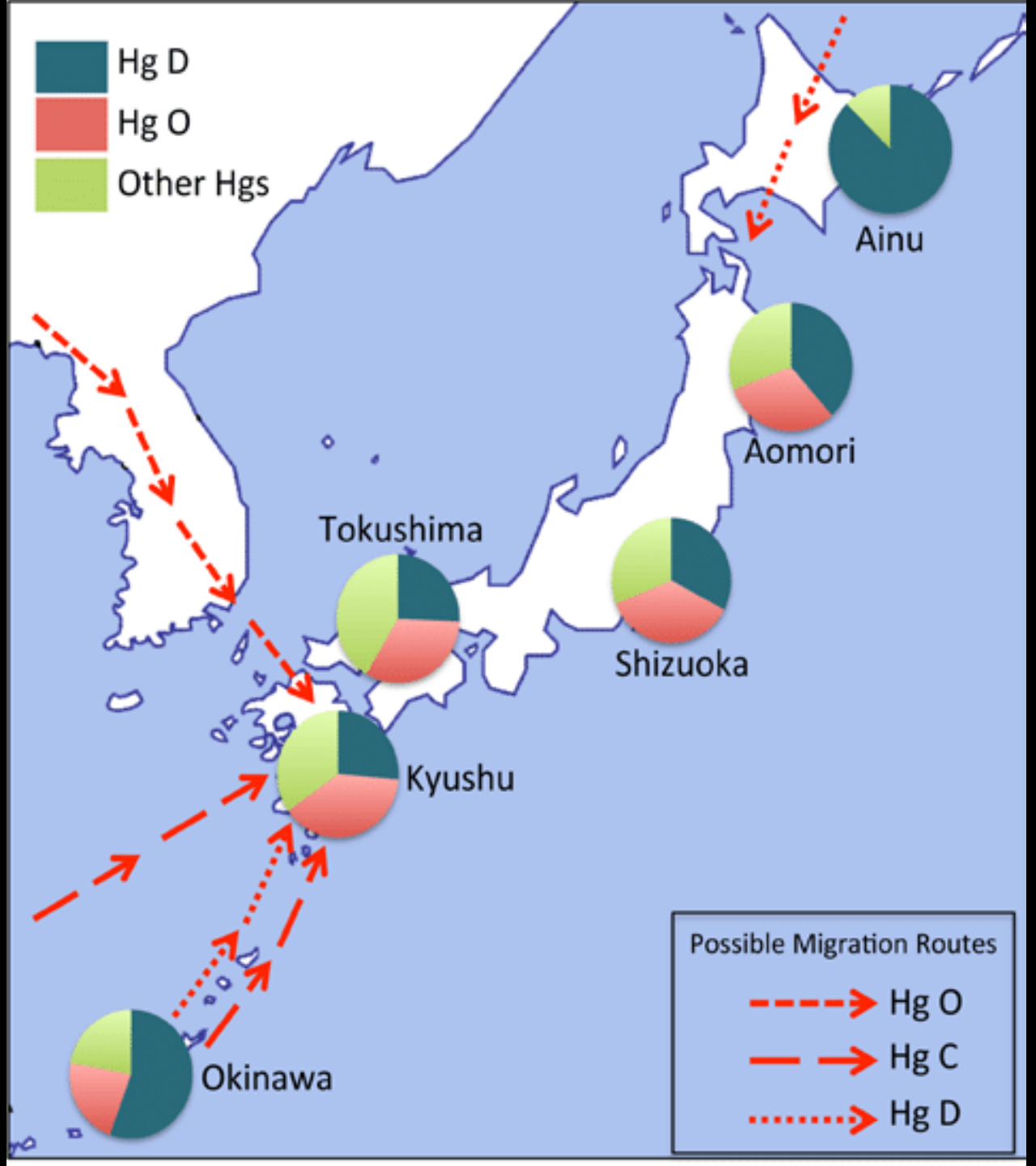
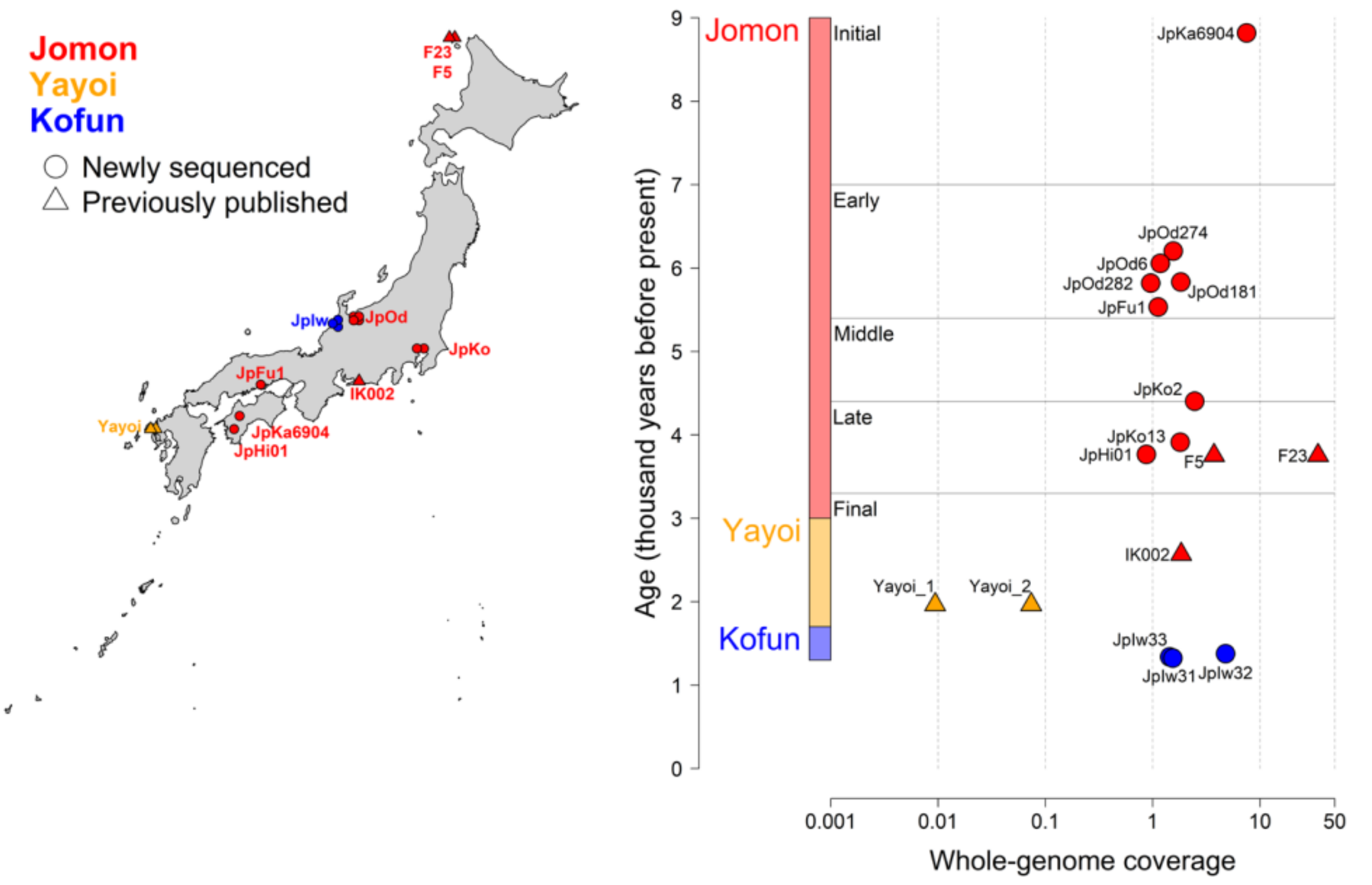
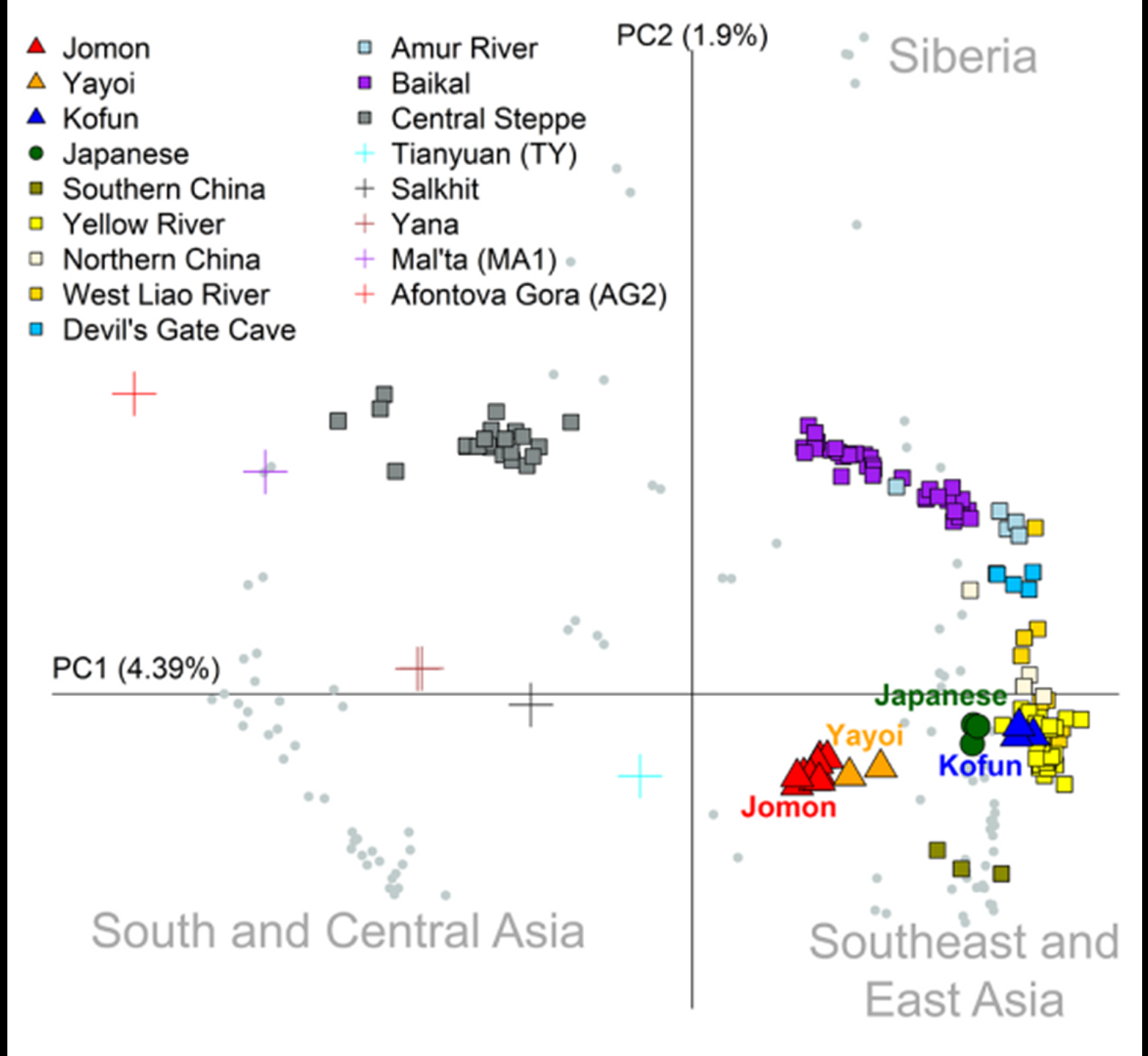
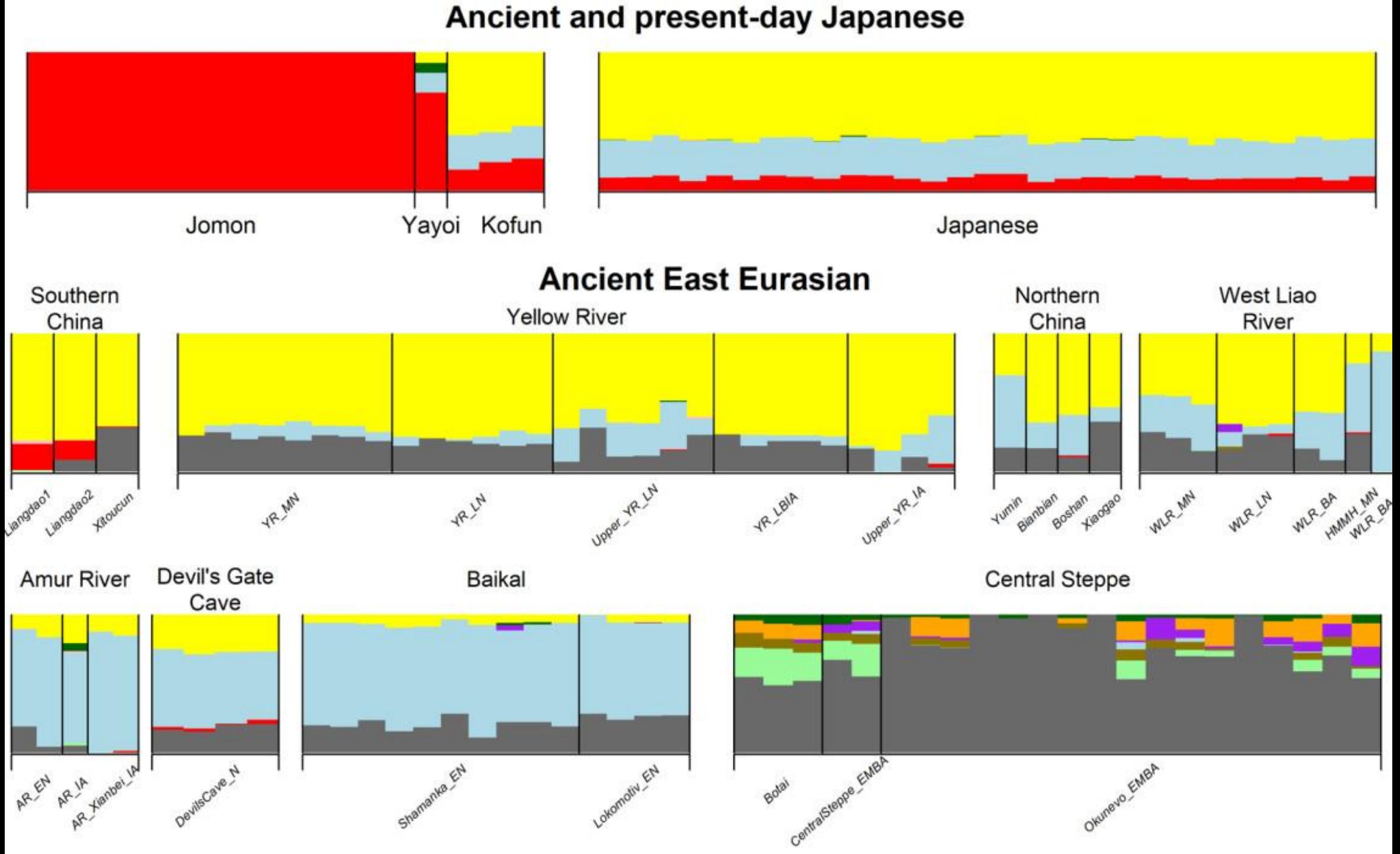
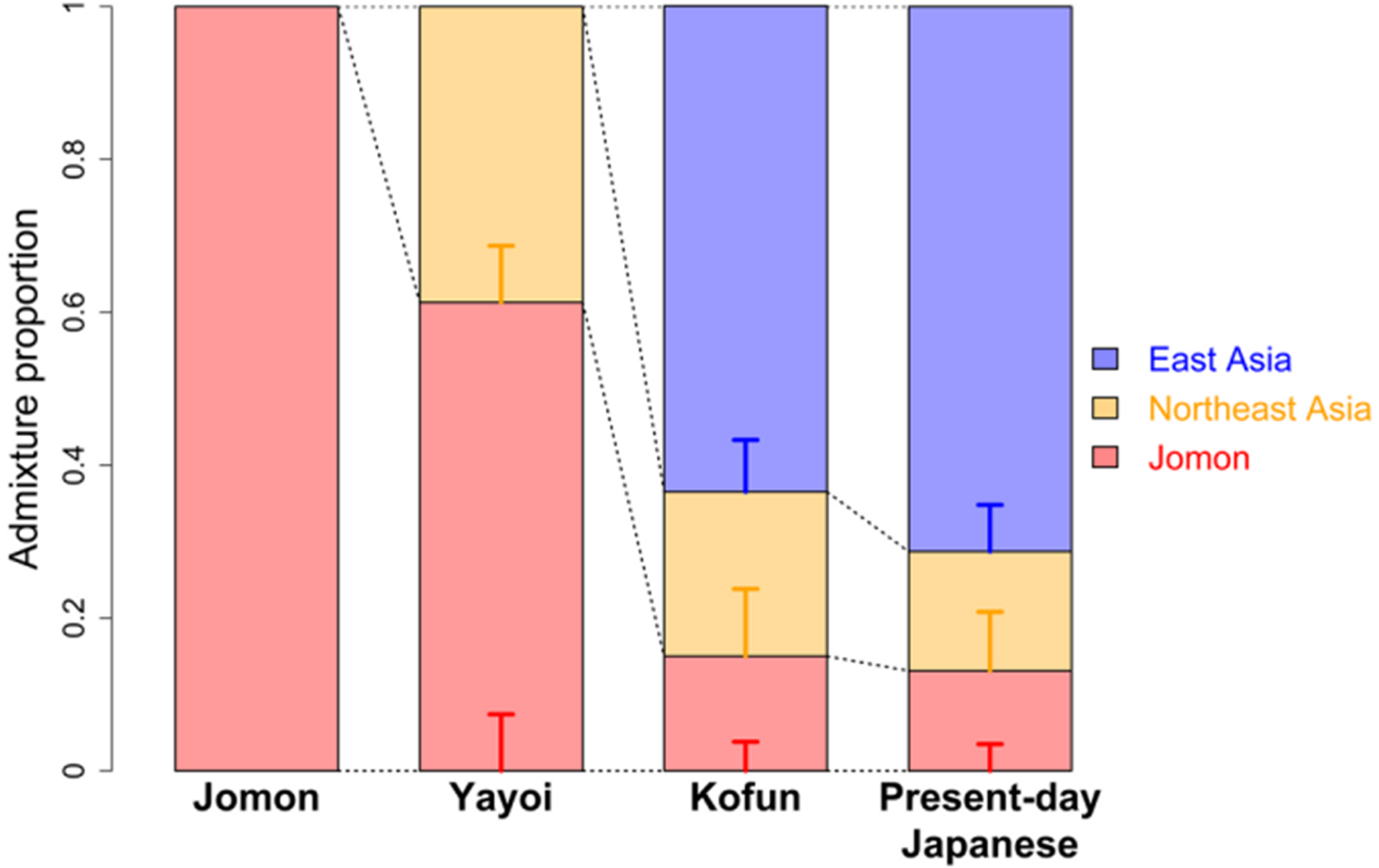
JAPAN GENEALOGICAL GENETICS
mt-DNA

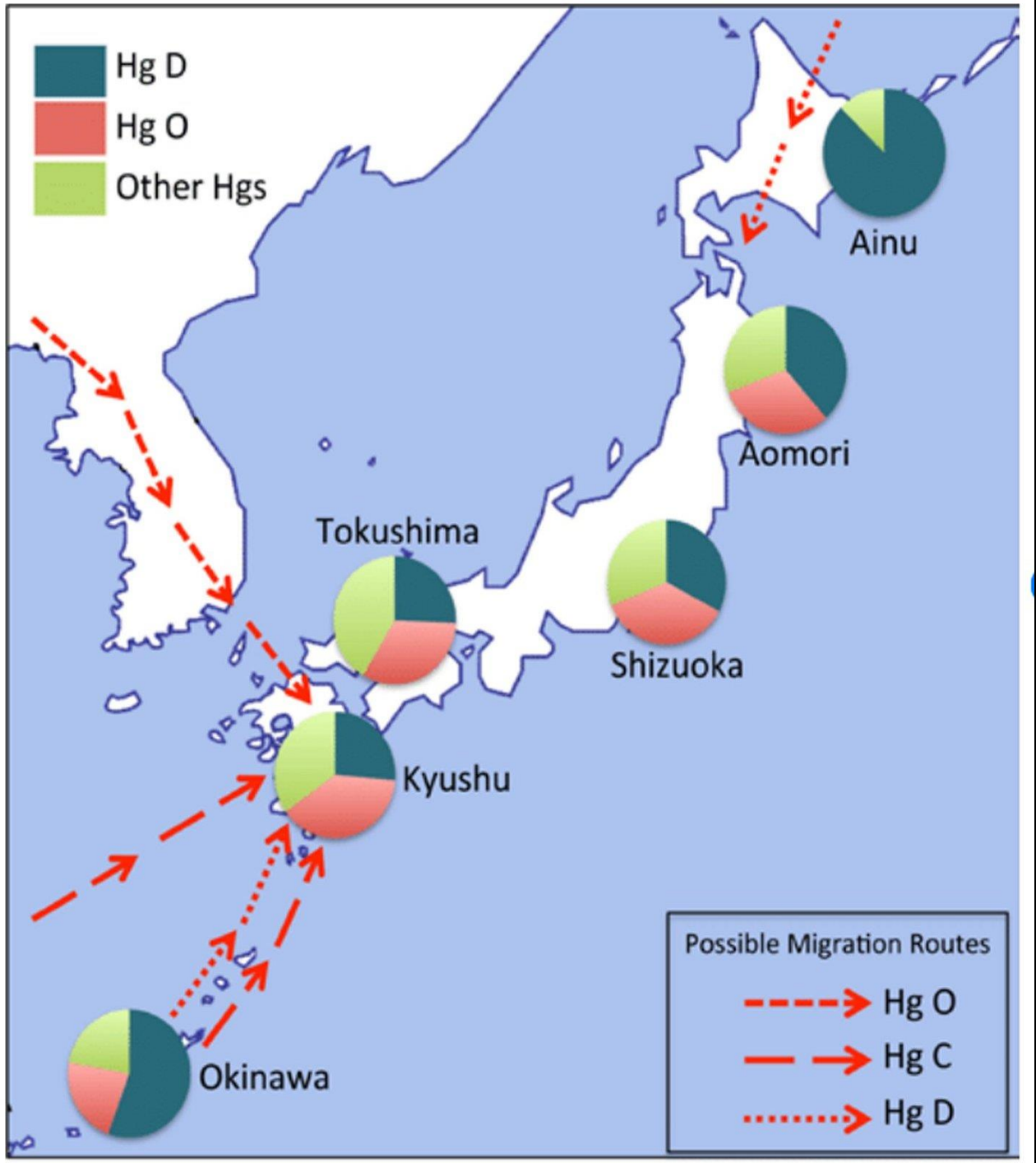

Hg D
Hg O
Other Hgs
Ainu
Aomori
Tokushima
Shizuoka
Kyushu
Okinawa
Possible Migration Routes
Hg O
Hg C
Hg D


Jomon
Yayoi
Kofun
Newly sequenced
Previously published
F23
F5
JpIw
JpOd
JpKo
JpFu1
IK002
Yayoi
JpKa6904
JpHi01
Age (thousand years before present)
Initial
Early
Middle
Late
Final
JpKa6904
JpOd274
JpOd6
JpOd282
JpOd181
JpFu1
JpKo2
JpKo13
JpHi01
F5
F23
IK002
Yayoi_1
Yayoi_2
JpIw33
JpIw31
JpIw32
0.001
0.01
0.1
1
10
50
Whole-genome coverage


Jomon
Yayoi
Kofun
Japanese
Southern China
Yellow River
Northern China
West Liao River
Devil's Gate Cave
Amur River
Baikal
Central Steppe
Tianyuan (TY)
Salkhit
Yana
Mal'ta (MA1)
Afontova Gora (AG2)
PC2 (1.9%)
PC1 (4.39%)
Siberia
Japanese
Yayoi
Kofun
Jomon
South and Central Asia
Southeast and East Asia


Ancient and present-day Japanese
Jomon
Yayoi
Kofun
Japanese
Ancient East Eurasian
Southern China
Liangdao1
Liangdao2
Xitoucun
Yellow River
YR_MN
YR_LN
Upper_YR_LN
YR_LBIA
Upper_YR_IA
Northern China
Yumin
Bianbian
Boshan
Xiaogao
West Liao River
WLR_MN
WLR_LN
WLR_BA
HMMH_MN
WLR_BA
Amur River
AR_EN
AR_IA
AR_Xianbei_IA
Devil's Gate Cave
DevilsCave_N
Baikal
Shamanka_EN
Lokomotiv_EN
Central Steppe
Botai
CentralSteppe_EMBA
Okunevo_EMBA


Admixture proportion
0
0.2
0.4
0.6
0.8
1
Jomon
Yayoi
Kofun
Present-day Japanese
East Asia
Northeast Asia
Jomon


Hg D
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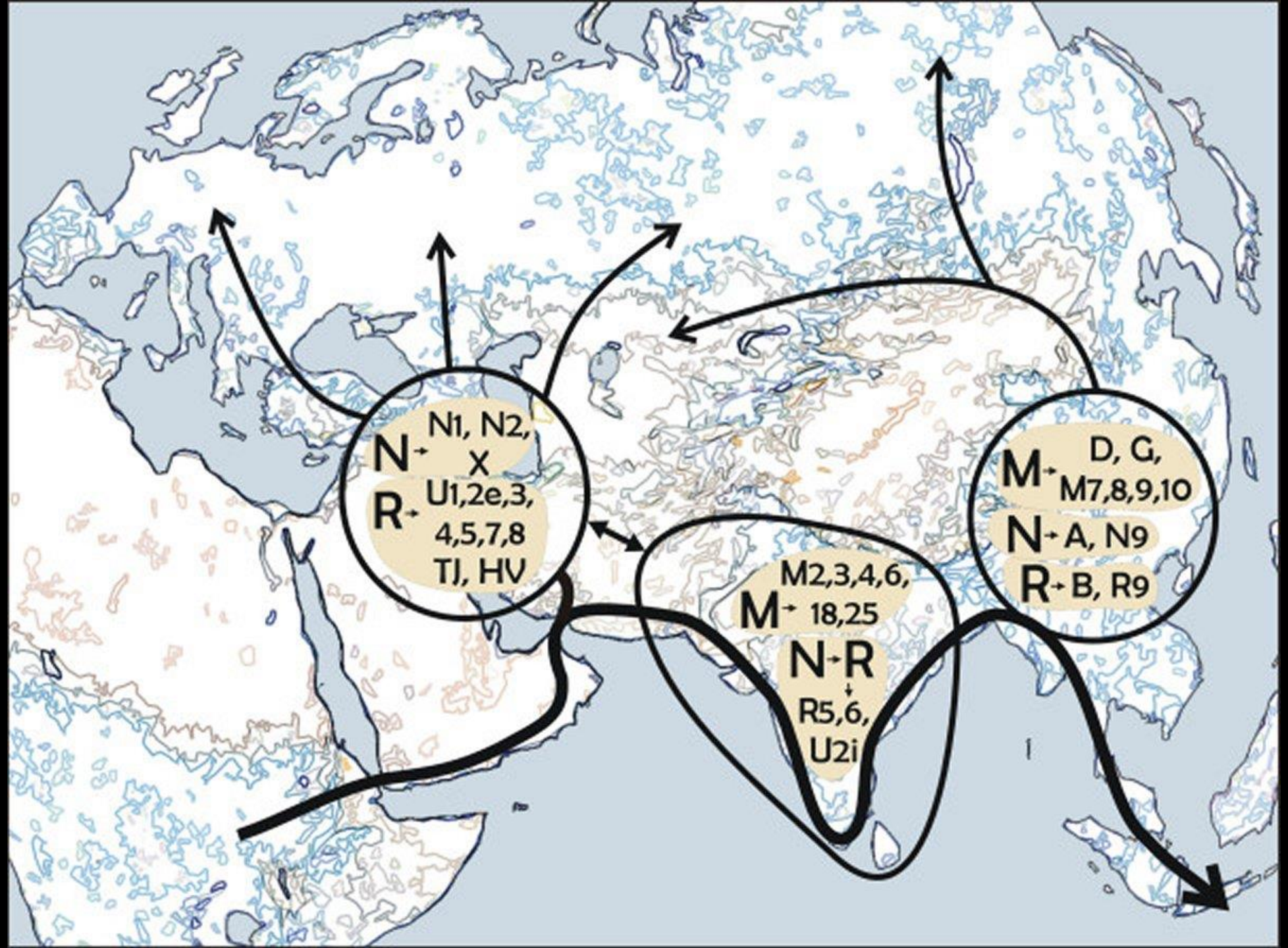
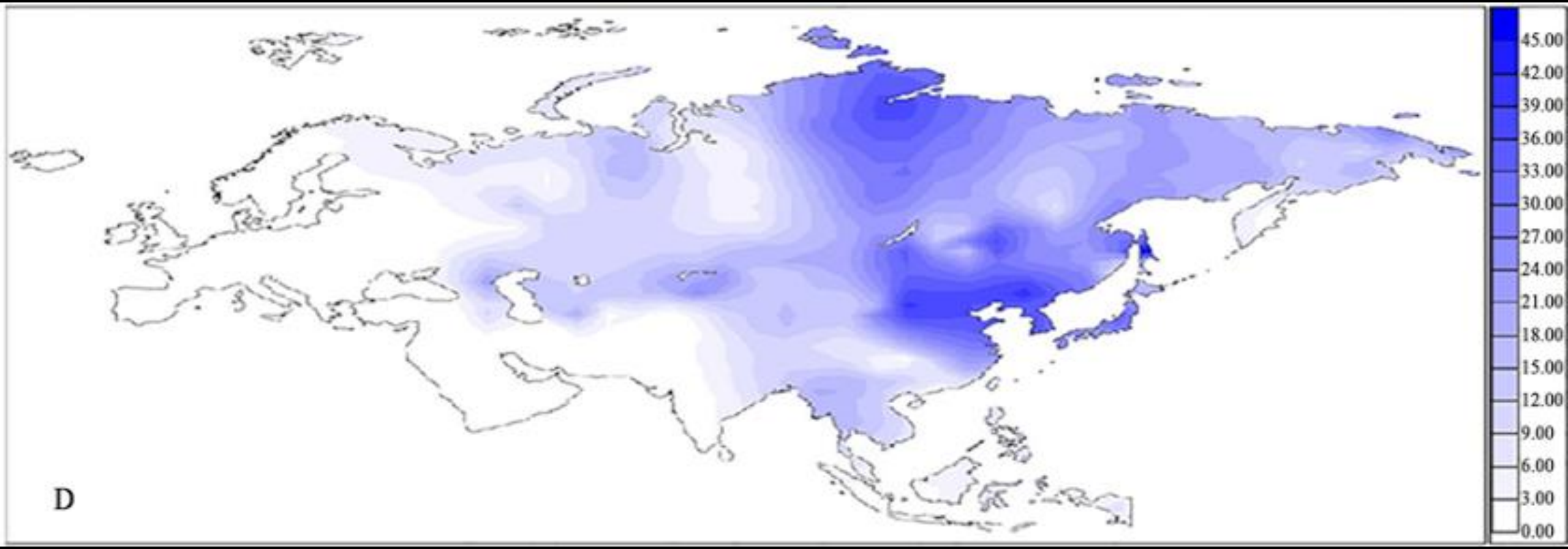
Possible Migration Routes
Hg O
Hg C
Hg D


N→ N1, N2, X
R→ U1,2e,3, 4,5,7,8 TJ, HV
M→ M2,3,4,6, 18,25
N→R
R5,6, U2i
M→ D, G, M7,8,9,10
N→ A, N9
R→ B, R9


45.00
42.00
39.00
36.00
33.00
30.00
27.00
24.00
21.00
18.00
15.00
12.00
9.00
6.00
3.00
0.00
D

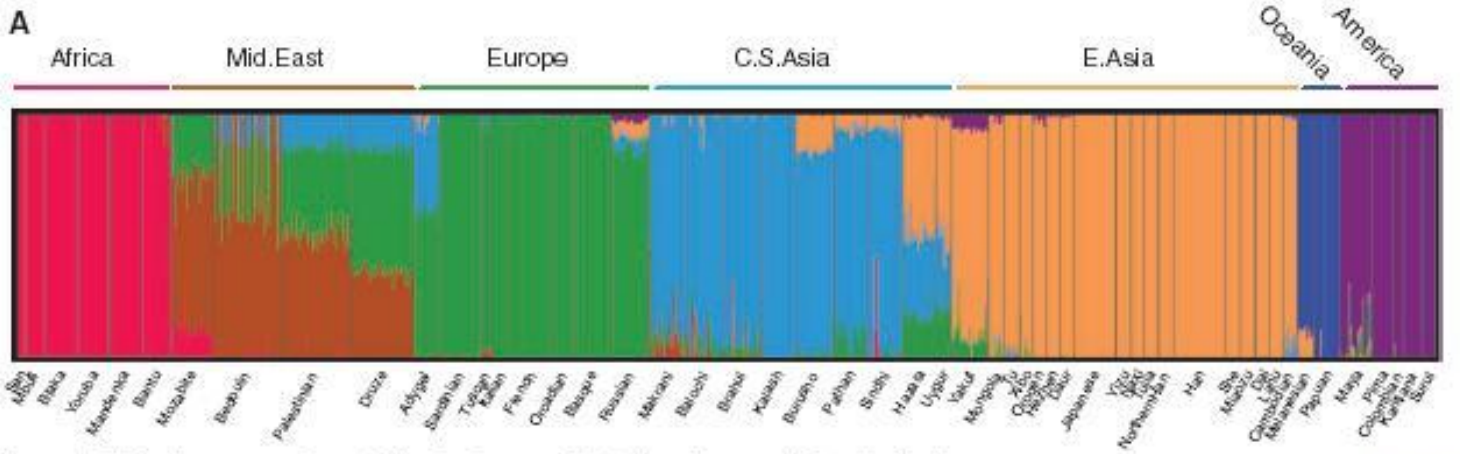
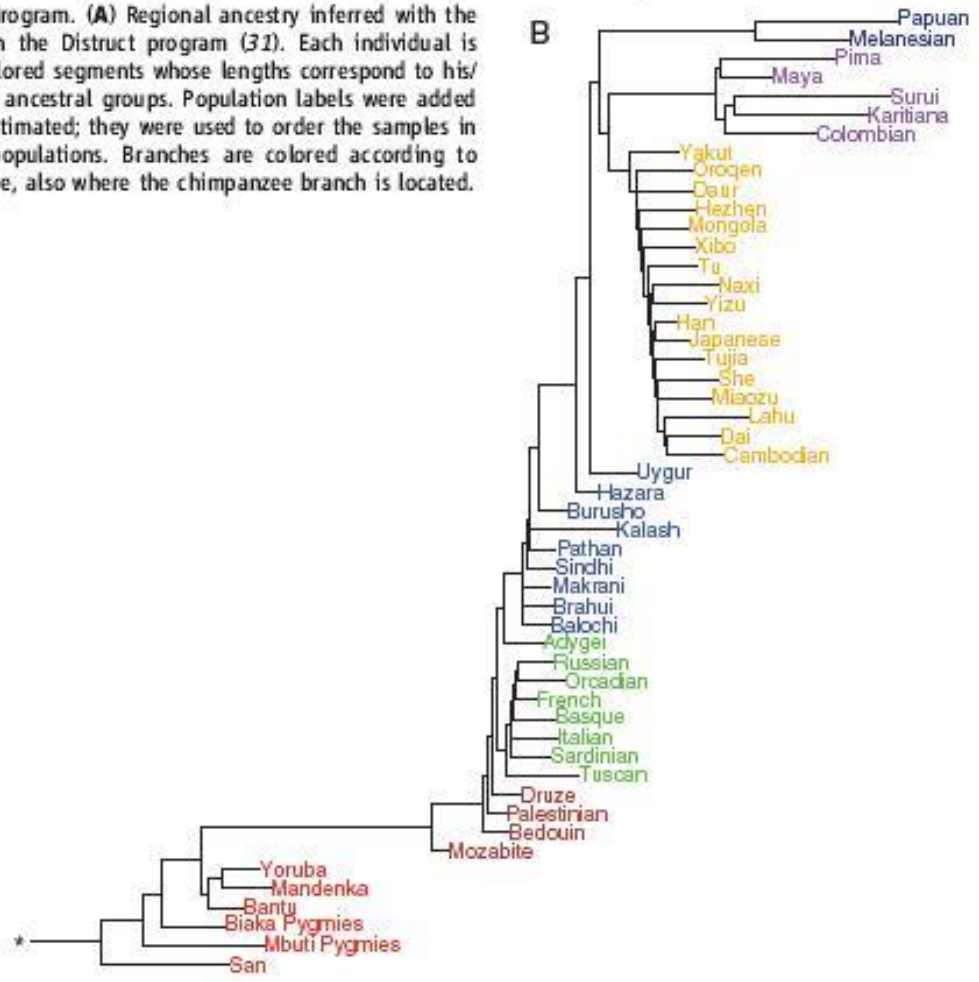
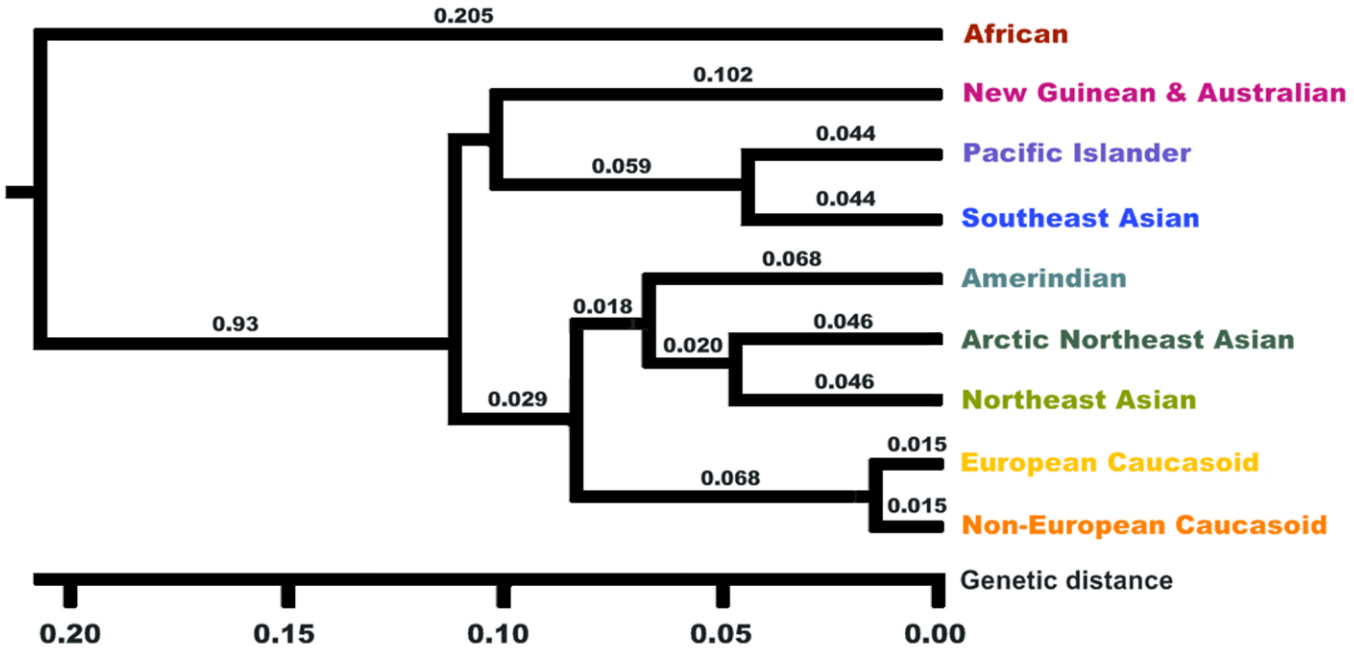


Fig. 1. Individual ancestry and population dendrogram. (**A**) Regional ancestry inferred with the *frappe* program at $K = 7$ (*13*) and plotted with the Distruct program (*31*). Each individual is represented by a vertical line partitioned into colored segments whose lengths correspond to his/her ancestry coefficients in up to seven inferred ancestral groups. Population labels were added only after each individual's ancestry had been estimated; they were used to order the samples in plotting. (**B**) Maximum likelihood tree of 51 populations. Branches are colored according to continents/regions. * indicates the root of the tree, also where the chimpanzee branch is located.



Linkage tree for 9 population clusters showing genetic distances (F_{ST})

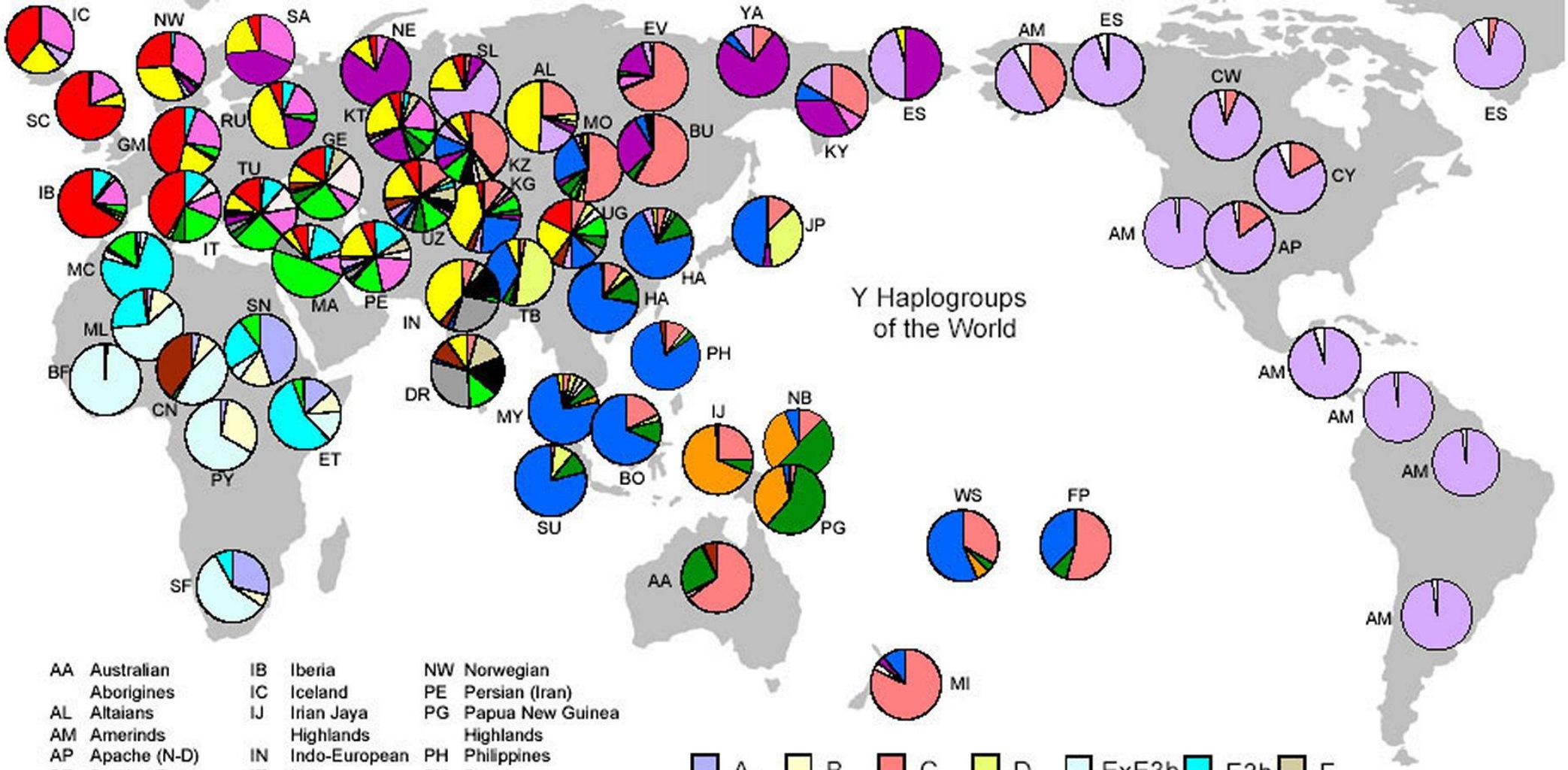
(Cavalli-Sforza *et al.*, 1994:80)



F_{ST} distance matrix for the 9 clusters shown above

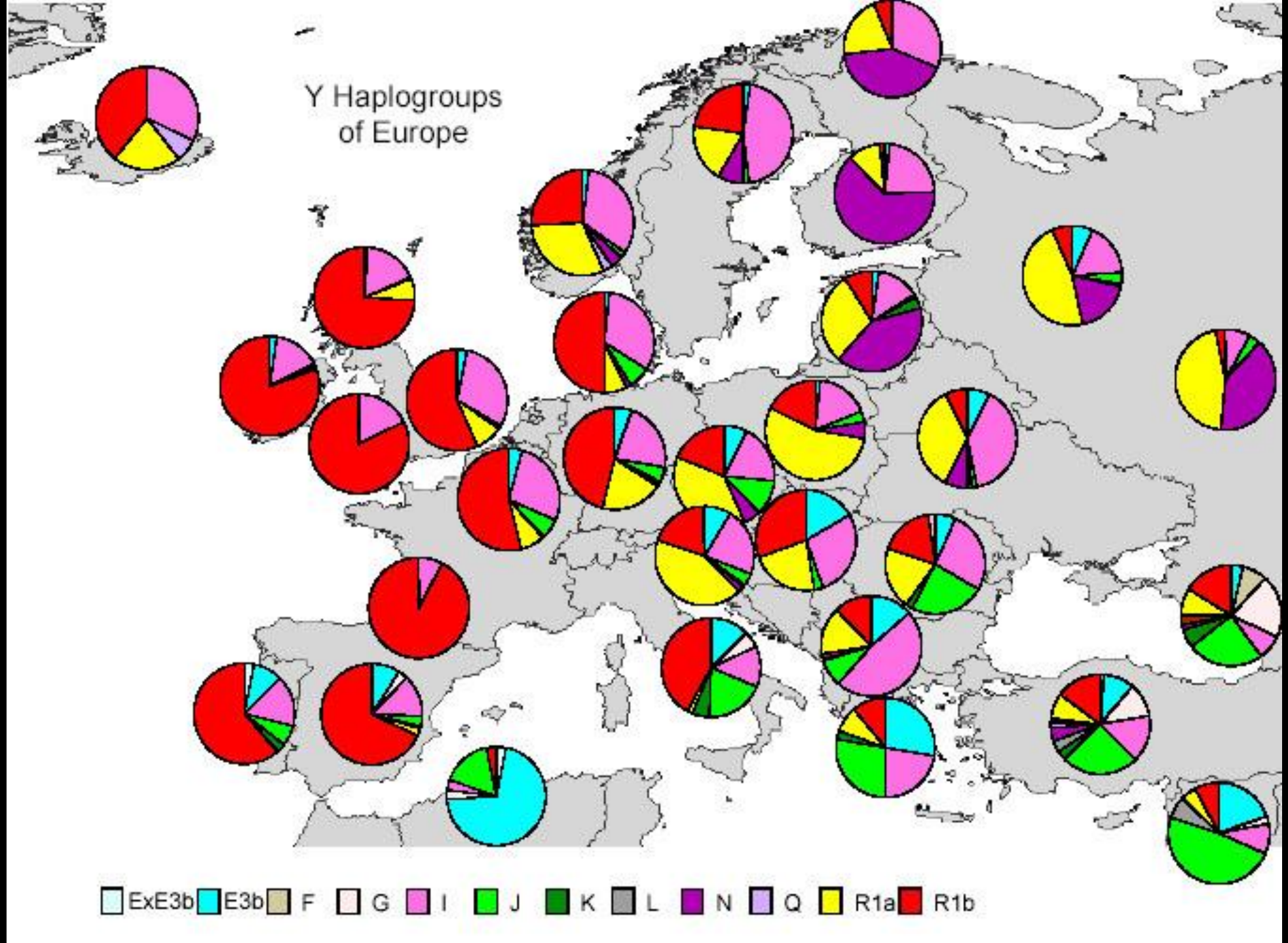
(x10,000 with standard errors obtained by bootstrap analysis)

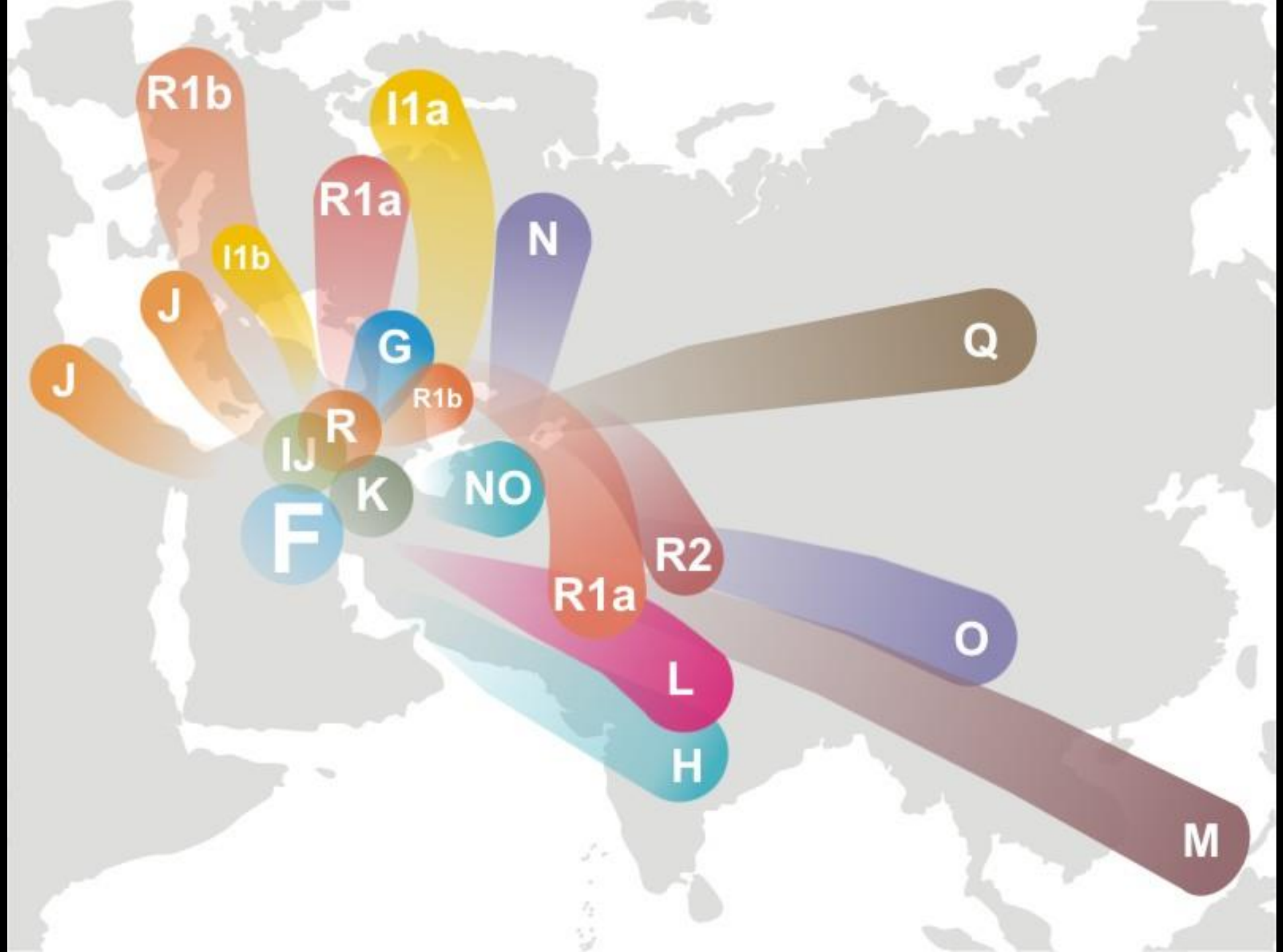
	AFR	NEC	EUC	NEA	ANE	AME	SEA	PAI	NGA
African	0.0								
Non-European Caucasian	1340.0 ± 301	0.0							
European Caucasian	1655.6 ± 416	154.7 ± 29	0.0						
Northeast Asian	1979.1 ± 452	640.4 ± 134	938.2 ± 217	0.0					
Arctic North-east Asian	2008.5 ± 387	708.2 ± 160	746.7 ± 210	459.7 ± 98	0.0				
Amerindian	2261.4 ± 434	955.5 ± 204	1038.2 ± 276	746.5 ± 183	577.4 ± 89	0.0			
Southeast Asian	2206.3 ± 529	939.6 ± 262	1240.4 ± 339	630.5 ± 299	1039.4 ± 326	1341.7 ± 418	0.0		
Pacific Islander	2505.4 ± 648	953.7 ± 230	1344.7 ± 354	723.8 ± 262	1181.2 ± 331	1740.7 ± 544	436.7 ± 87	0.0	
New Guinean and Australian	2472.0 ± 536	1179.1 ± 189	1345.7 ± 231	734.4 ± 118	1012.5 ± 257	1457.9 ± 283	1237.9 ± 277	808.7 ± 264	0.0



AA	Australian Aborigines	IB	Iberia	NW	Norwegian
AL	Altaians	IC	Iceland	PE	Persian (Iran)
AM	Amerinds	IJ	Irian Jaya Highlands	PG	Papua New Guinea Highlands
AP	Apache (N-D)	IN	Indo-European	PH	Philippines
BF	Burkina Faso	IT	Italy	PY	Pygmy
BO	Borneo	JP	Japan	RU	Russia
BU	Buryats	KG	Kyrgyzstan	SA	Saami
CN	Cameroon	KT	Kazan Tatar	SC	Scotland
CW	Chippeway (N-D)	KY	Koryaks	SL	Selkups
CY	Cheyenne	KZ	Kazakhstan	SF	South Africa
DR	Dravidian	MA	Mideast Arabs	SN	Sudan
ES	Eskimos	MC	Morocco	SU	Sumatra
ET	Ethiopia	MI	Maori	TB	Tibet
EV	Evenks	ML	Mali	TU	Turkish
FP	French Polynesia	MO	Mongols	UG	Uygurs
GE	Georgia-Armenia	MY	Malaysia	UZ	Uzbek
GM	Germany	NB	New Britain	WS	Western Samoa
HA	Han Chinese	NE	Nenets	YA	Yakuts

The data in this map is supposed to represent the situation before the recent European expansion beginning about 1500 AD. In some cases such as some Native American tribes and the Maori this can be done reliably because STR typing was done. In other cases, especially in America, it is guesswork. The "Other" sectors in America indicate this. Native American groups are labeled by language group as Amerind, Na-Dene (N-D), and Eskimo. F, K, L, and P are in some cases "catchall" groups because some researchers did not use enough markers for a full haplotype determination.


Y Haplogroups
of Europe
ExE3b
E3b
F
G
I
J
K
L
N
Q
R1a
R1b


R1b
I1a
R1a
N
I1b
J
Q
G
J
R1b
R
IJ
K
NO
F
R2
R1a
O
L
H
M